Figure S1 Correlation of I_a and PC1 weight values of the 5,000 AIMs. The PC1 weight values of the AIM markers were calculated using the "snpweightoutname" function implemented in the EIGENSOFT package[16](http://genepath.med.harvard.edu/~reich/Software.htm). I_a of each of the 5,000 SNPs is highly correlated with its eigenvector weight of PC1 (r=0.947). The horizontal axis represents Log(I_a); The vertical axis represents Log(|PC1|).